

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 30, 2001, 04:14:06 ; Search time 1386.2 Seconds  
(without alignments)  
11790.495 Million cell updates/sec

Title: US-09-403-262A-1  
Perfect score: 1729  
Sequence: 1 cctcgtccctcccccagcag.....ctattttattttaatca 1729

Scoring table: IDENTITY\_NIC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
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255: gb\_est186:\*  
256: gb\_est187:\*  
257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.



University of Minnesota  
495 Boylsg Hall, 1991 Upper Buford Circle, St. Paul, MN 55108, USA  
Tel: 612 625 1243  
Fax: 651 649 5058  
Email: debbys@specnicr1.crl.umn.edu  
Minnesota sequence name: M260125e  
ILIR sequence name: MTFB437K  
More information is available at:  
<http://chryslr.tamu.edu/mediago>  
Seq primer: Skmcd / CTA gga CTA gtc gat CC).

FEATURES	Location/Qualifiers
source	1. .717

```
1..717
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pBSIL-12H13"
/clone_1b="BSIL"
/tissue_type="leaves infected with Colletotrichum
trifolii"
```

```

/dev/stage="cotyledons and primary leaves harvested 5 and
8 days after inoculation with Colletotrichum trifolii"
/Lab host="E. coli strain K10UR"
/note="vector: pluscript SK+, Site_1: EcoRI, Site_2:
XhoI, cDNA was prepared from polyA+ enriched RNA from
cotyledons and primary leaves harvested 5 and 8 days after
inoculation with Colletotrichum trifolii. The cDNA was
directionally ligated into the uni-TAP XR vector from
stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-TAP phase using Ex-8000
helper phase and propagated in K10UR cells. Note: EST may
be of fungal origin."

```

BASE COUNT	217 a	121 c	165 g	214 t
ORIGIN				

Query Match	6.38;	Score 109;	DB 123;	Length 717;
Best Local Similarity	54.0%;	Pred. No. 2.8e-15;		
Matches 248;	Conservative	0;	Mismatches 205;	Indels 6; Gaps 1

QY	969	tttttcataaggtttaaataatgaacccaaatattgttaacatcgcgaaagaagacaa	1028
	1111	111	
Db	95	TTTTGAGATTGGTAAAGTCCTCTCTCCAAAGTGGTACCCCTTGTGACAAGATCAA	154
QY	1029	atcatatacaatcccttttttttcaagaattacagagcgcttgattatataacgcg	1088
	1111	111	
Db	155	ACACAACACAAACACCTTTCTTCACAGGTCATGAAATCTGACACTACTCTTGSCAA	214
QY	1089	tctttgattacactgaagacacacatgcccgcggatgcgagaagatgaacatgac	1148
	1111	111	
Db	215	TCTTGAGATCCATGATGATGACCCCTCTCAAGAAATGCAAGACGAGATTAATGTGAC	274
QY	1149	aagctgctgttttggagaagaaatgcttgatatacgttgcgaatgagaagatataaagaag	1208
	1111	111	
Db	275	AACATCTTTTGGCTCGGGATATCTGTCANATGCTATATGCTGTGAAGCAAGAAAGAGTGC	334
QY	1209	aaagacatgaagaagttaatacatcattggaagaaatgcttgaagagatctgattagtaacg	1268
	1111	111	
Db	335	AGCGACACGAACCTGTTTGGTAAGTGGGAATCTCAGTGTATACATATCCGGGATTTTCGCAAT	394
QY	1269	ttgccttaagcccttttgaattatcaaaagctaacgtctcttttgaagcttcaattacctt	1328
	1111	111	
Db	395	GTCTCTTAACTTAAATGTAATTCCTGTTATTAAGAAGCGCTTCTAAG-----TGTATT	448

OY	1329	cTgaagcgtcaactcgagattcgagaatcttcttccttgtagttgcaaaacac	1388
Dd	449	CAGACGACTATTCACCTAGTTGGAGAAGATGGGCACAATCCTTAGGTGGAAAGCAGAA	508
OY	1389	ccctttcccatctcgcgcttggttggaataacct	1427
Dd	509	ATTTGATATTCGCTTCAGCTTGGATGATGAACAAT	547

RESULT	3
LOCUS	Bf219552/c
DEFINITION	Bf219552 700 bp mRNA EST O6-NOV-2000 GM070018A10H11 Gm-r1070 Glycine max cDNA clone Gm-r1070-7569 3'
ACCESSION	Bf219552 Bf219552 Bf219552.1 GI:1117959
VERSION	EST.
KEYWORDS	soybean.
SOURCE	Glycine max
ORGANISM	

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 700)	Vodkin, L., Keim, P., Shoemaker, R., Retzel, E., Khanna, A., Corryell, V., Erding, J., Rapp, C., Shoop, E., Pardinas, J., Liu, L. and Lewin, H.	A Functional Genomics program for Soybean (NSF 9872565)	Unpublished (1999)	Other ESTs: AW308889 corresponding to Gm-c1019-3436 (5')

COMMENT  
Other ESTs: AW308889 corresponding to Gm-c10109-496 (5')  
Contact: Vodin, L.O., PI, A Functional Genomics Program for  
Soybean (NSF 9872655)  
Lewin, H. A., Director, Keck Center for Comparative and Functional  
Genomics  
University of Illinois  
Edwin R. Madigan Building, 1201 W. Gregory, Urbana, IL 61801, USA  
Tel: (217) 244-6147  
Fax: (217) 333-4582  
Email: l-vodkin@uiuc.edu  
This clone is available through: Genome Systems, Inc. 4633 World  
Parkway Circle St. Louis, Missouri 63134. For further information  
call: (800) 430-0030 or (314) 427-3322 Fax: (888) 919-3324 or (314)  
427-3324 or contact: clones@genomesystems.com or Info@genome  
systems.com web site: www.genomesystems.com  
Seq primer: 5'-TTTTTTTTTTTTT(A/C/G)-3'.

FEATURES	Location/Qualifiers
source	1. . 700

`/organism="Glycine max"
/db_xref="taxon:3847"
/clone="Gm-r1070-7269"
/clone_id="Gm-r1070"
/notes="The library Gm-r1070 is a sequence-driven, rerecked set of 9,216 clones selected from cDNA libraries from various tissues and stages of development of soybean that represent 2,639 sequences from immature cotyledons, 1,770 from immature seed coats, 3,938 from flowers, and 869 from young pods. The 5' ESTs of the source clones from the different libraries was used to select singletons, or a representative of each contig, which were rerecked to form library Gm-r1070. The cDNA clones of the rerecked Gm-r1070 library were then sequenced at the 3' end. The contig analysis to select unique genes was performed by the laboratory of Ernest Reizel, Center for Computational Genomics and Bioinformatics, University of Minnesota, http://www.cbc.umn.edu/ResearchProjects/Soybean/index.html. Rerecking was performed by Genome Systems, St. Louis, http://www.genomesystems.com, and 3' sequencing by the Reck Center for Comparative and Functional Genomics, University of Illinois, http://www.life.uiuc.edu/bioreck/reck.html. Note: The corresponding 5' EST from each clone in the Gm-r1070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of`

the original cDNA library that is also listed under 'OTHER EST's'

BASE COUNT 182 a 165 c 127 g 201 t 25 others  
ORIGIN

Query Match 6.3%; Score 108.6; DB 146; Length 700;  
Best Local Similarity 57.1%; Pred. No. 3.5e-15;  
Matches 198; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 977 agggtaagtaacgaaccccaaatgltacatcgcgcgaagaagaacatacatc 1036  
DB 585 ATGGTTAGAGCTGAATCCAAAATTTGTGACAGTTGTGAGACGAGCATGACCAAC 526  
QY 1037 catcctcttttttacaagaatcgcgagcggttgatttatacagctgtgttgat 1096  
DB 525 ACCCTCCCTTTTCCTCCAGATTCATGTAACCTCAATTCCTGCTGTGTTAC 466  
QY 1097 tcactgagagctacatgcccgcggtagtcgagagagagatgacagttgaacagtg 1156  
DB 465 ACACCTGATGCACTCTCCCAAGGAGAGCCAGACAGATGATGTGAAAGCAATGC 406  
QY 1157 ttgggaagaagatgtgtatatacgttcgataaggaagataaaaggaagaacat 1216  
DB 405 CTGCAAAAGACATTTGCAACATTTGTCATGTGAGGGCGAAGAAAGAACGGTAT 346  
QY 1217 gaaaggttagatcatggaagatgattgagagagttgagattagtaatgtgtctta 1276  
DB 345 GAAGTCGCCGGAATAATGAGGCGGAGTTGTCAGTGGCTTCCTCCTCCATTCG 286  
QY 1277 agccctttgcatatatacgaagcttctttgagatcttca 1323  
DB 285 AGCACAATGTGAGNAGCAATTAAGCATCTCATTTAAGCAATA 239

RESULT 4  
LOCUS BG587603 645 bp mRNA EST 11-APR-2001  
DEFINITION EST489377 MHAM Medicago truncatula/Glomus versiforme mixed EST  
ACCESSION BG587603  
VERSION BG587603.1 GI:13602667  
KEYWORDS EST.  
SOURCE Medicago truncatula/Glomus versiforme mixed EST library.  
ORGANISM Medicago truncatula/Glomus versiforme mixed EST library.  
REFERENCE 1 (bases 1 to 645)  
AUTHORS Eukaryota: mixed EST libraries.  
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.  
and Fraser,C.M.  
ESTs from roots of Medicago truncatula after colonization with  
Glomus versiforme, 2001  
TITLE Unpublished (2001)  
JOURNAL Contact: Harrison M.J.  
COMMENT Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401  
Tel: 580-223-5810  
Fax: 580-221-7360  
Email: mharrison@noble.org  
Noble EST name: N38675e TIGR sequence name: MTDD129TK More  
information is available at: http://www.medicago.org  
Seq primer: SKmod (CTA gaa cta gtc gat cc).  
Location/Qualifiers  
1. 645  
/organism="Medicago truncatula/Glomus versiforme mixed EST  
library"  
/cultivar="Medicago truncatula genotype A17"  
/db\_xref="taxon:119092"  
/clone="PMHAM-50F9"  
/clone\_id="MHAM"  
/tissue\_type="roots colonized with Glomus versiforme"  
/dev\_stage="Roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glomus versiforme. The library was

made from a mixture of RNA from each of these stages."  
/lab\_host="E. coli strain XL0LR"  
/note="Vector: pBluescript SK-; Site-1: EcoRI; Site-2:  
XhoI; cDNA was prepared from polyA+ enriched RNA from  
roots harvested at 10, 17, 22, 31 and 38 days  
post-inoculation with Glomus versiforme. The cDNA was  
directionally ligated into the unizap XR vector from  
Stratagene and packaged using Gigapack III Gold packaging  
extracts. Plasmids containing cDNA inserts were excised  
from the recombinant lambda-zap phage using Ex-assist  
helper phage and propagated in XL0LR cells."

BASE COUNT 191 a 136 c 158 g 160 t  
ORIGIN

Query Match 6.2%; Score 107.2; DB 155; Length 645;  
Best Local Similarity 60.1%; Pred. No. 7.4e-15;  
Matches 178; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 969 tttagataggttaagtaacatgaacccaataatgttacaatcgcgagaagaacaa 1028  
DB 280 TTTCCGATGTTAAGAGCCTTAATCCAAAATTTGTAAGTTGTGAACAAAGAGTG 339  
QY 1029 atcataaccatccctctttttacaagaatcatcgagcggttgattatatacagctg 1088  
DB 340 ACACAAACNCTTCCCATTTCTTCCAAAGATTTGTTGAAGCTTACATTAATCTGCTG 399  
QY 1089 tgttgatcactggaagctacatgcccagcggtagtcgagagaagatgacagttgaac 1148  
DB 400 TGTGTAGTCCCTTGACCCACTCTTCCGAGAGACATCAAGATGAGTGAATGTTGAA 459  
QY 1149 aagtggtttgggagaagaattgtgatcgttgatgagatgagaagataaagaag 1208  
DB 460 GCCAATGCTTGGCGGAGGACATTTGAAATGTCATTCGCGAGGCGACGATGAAGA 519  
QY 1209 aaagacatgaaggttagatcatggaagtatgtgaggaagttgagattagt 1264  
DB 520 AAAGTATGAAGCTCCCTGGAATAATGAGGCGCAAGATGAATAATGCTGATTCACT 575

RESULT 5  
LOCUS BG587606 772 bp mRNA EST 12-APR-2001  
DEFINITION EST490515 MHRP- Medicago truncatula cDNA clone pmHRP-57620, mRNA  
ACCESSION BG587606  
VERSION BG587606.1 GI:13606846  
KEYWORDS EST.  
SOURCE barrel medic.  
ORGANISM Medicago truncatula  
REFERENCE 1 (bases 1 to 772)  
AUTHORS Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.  
Harrison,M.J., Liu,J., Town,C.D., Van Aken,S., Uterback,T., Cho,J.  
and Fraser,C.M.  
ESTs from phosphate-starved roots of Medicago truncatula, 2001  
TITLE Unpublished (2001)  
JOURNAL Contact: Harrison M.J.  
COMMENT Plant Biology Division  
The Samuel Roberts Noble Foundation  
2510 Sam Noble Parkway, Ardmore, OK 73401  
Tel: 580-223-5810  
Fax: 580-221-7360  
Email: mharrison@noble.org  
The Samuel Roberts Noble Foundation: N387457e TIGR sequence name:  
MTHBD22TK More information is available at: http://www.medicago.org  
Seq primer: SKmod (CTA gaa cta gtc gat cc).  
Location/Qualifiers  
1. 772  
/organism="Medicago truncatula"  
/cultivar="A17"  
/db\_xref="taxon:13880"

FEATURES  
source

BASE COUNT  
ORIGIN

238 a 134 c 174 g 226 t

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/clone="pMHRP-57C20"  
/clone_1b="MHRP-n"  
/tissue_type="roots"  
/dev_stage="phosphate-starved"  
/lab_host="XLOLR"  
/note="Vector: bluescript SK-, Site_1: EcoRI; Site_2:  
xhoI; At the trifoliolate stage, M. truncatula plants were  
transplanted to phosphate-free sand and grown for a  
further 30 days. During this period, they were fertilized  
twice weekly with 1/2 Hoaglands solutions containing 20mM  
potassium phosphate. cDNA was prepared from polyA+  
enriched RNA. The cDNA was directionally ligated into the  
Unisap XR vector from Stratagene and packaged using  
GigaPack III Gold packaging extracts. Plasmids containing  
cDNA inserts were excised from the recombinant lambda-zap  
phage using Ex-assist helper phage and propagated in  
XLOLR cells."
```

Query Match	6.28;	Score 107.2;	DB 155;	Length 772;
Best Local Similarity	60.18;	Prod. No. 7.6e-15;		
Matches 178;	Conservative	0;	Mismatches 118;	Indels 0;
			Gaps	0;
Qy 969	tttgcattagaggttaagatcaatgacccctaacaattgttacaatcgcgcgaggaagca	1028		
Ddb 63	ttctccgcatggttttagagccttatcccaaaccttgtaacagttggaacagagtgta	122		
Qy 1029	atcataaccatcctcttttttacaagaattcacgagcggttggtttattacagctg	1088		
Ddb 123	acacaaacacacttccccatttctccaaattggttgaaagctttacatttactactcgcg	182		
Qy 1089	tgtttgattcacttggaagctacattgcaccgcggtagtcgagagagatgacagttgaac	1148		
Ddb 183	tgttttagtcccttgacgcctactcttccgagagagatgcaagatagagctgaattgaaa	242		
Qy 1149	aagtgcggttttgagagagattgttgatatcgttgcgatgagagagataaagaagaa	1208		
Ddb 243	ggcaatgccttgaggagagacatttgaaatgctattgcttgccgagggcgagagatgaaatag	302		
Qy 1209	aaagacatgaaaggttttagatcatcgtggaagtatgttgaagagtttgattagt	1264		
Ddb 303	aaagatgtgaatgcctgcaaaatgagagcgcaagatgaaatggctgattcact	358		

RESULT	6			
LOCUS	BG443698	671 bp	mrna	EST
DEFINITION	GA_Ea0021107f Gossypium arboreum 7-10 dpa fiber library Gossypium			15-MAR-2001
ACCESSION	BG443698			
VERSION	BG443698			
KEYWORDS	BG443698.1 GI:13353350			
SOURCE	EST.			
ORGANISM	Gossypium arboreum.			
REFERENCE	Gossypium arboreum.			
AUTHORS	Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
	Rosidae; eustosids II; Malvales; Malvaceae; Gossypium.			
TITLE	1 (bases 1 to 671)			
	Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry			
	, D., Wood, T.C., Leslie, A. and Wilkins, T.A.			
	An integrated analysis of the genetics, development, and evolution			
	of the cotton fiber			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Wing RA			
	Clemson University Genomics Institute			
	Clemson University			
	100 Jordan Hall, Clemson, SC 29634, USA			
	Tel: 864 656 7288			
	Fax: 864 656 4293			
	Email: rwing@clemson.edu			
	Seq primer: TATACGACTCATATAGCG			

FEATURES	
source	High quality sequence stop: 465.
Location/Qualifiers	
1. 671	
/organism="Gossypium arboreum"	
/strain="AKA"	
/cultivar="8400"	
/db_xref="taxon:29729"	
/clone="GA_Ea0021107f"	
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"	
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"	
/lab_host="E. coli"	
/note="vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"	
153 a 122 c 221 g 175 t	
BASE COUNT	
ORIGIN	

Query Match	6.1%;	Score 106;	DB 153;	Length 671;
Best Local Similarity	50.4%;	Pred. No. 1,4e-14;		
Matches 259;	Conservative	0;	Mismatches 255;	Indels 0;
OY 898	tgaacccctagcatcaactggtgtttcttaacctcaacgcgccttttaagaacgcgga	957		
DB 1	TGAAGTACTGACGGGTGAACCGCTGTTTTCAGAGCTTCACTCCCTGTGAGCTCGACCGGGTGG	60		
OY 958	gttaagatcttttttgcatatggtttaagtaaatgaacccataaatgtttacatcgcgga	1017		
DB 61	GATGCAAAAAGCTTTTCTCTCTATTAAGGATGAAACCCAGATGTGTCACGGTGTGGA	120		
OY 1018	gaaggaagcaaatcatataacacatccctcttttttacaagaatcaltcagaggttgatt	1077		
DB 121	ACAAAGAACGAAATCAACAACGGTCTCTGTTTCTTAAACCGCTTTTACTGAAGCTCTCCATTA	180		
OY 1078	ttatacagctggtgtttgatttaccggaagcttaaatgtccacggtatgtcgaagagat	1137		
DB 181	TTATCTCTACCCCTTTTCGACTGCTGTTGGAAAGTTCGGGGGTGGCCCAACGATCAAGACCT	240		
OY 1138	gacagcttgacaacagtgtgttttggagaagagattgttgatatacgttgagatggaagaga	1197		
DB 241	GCGTATGTCGAGGTATATCTTAGGAAGACAAATTTGTAACGTGGTGTCTGTGAAGGAT	300		
OY 1198	taaaagaaagaagaacatgaaagtttagatctcaggaagtattgttggagattgttgg	1257		
DB 301	GGACCCAGTGGAGCGACACAGACCCCTTACATCACTGGAGAACTCGATGAAACGGCCGG	360		
OY 1258	atttagtaatgttgcctttaagcccttttgcaattacacaagctaaagctcttttagact	1317		
DB 361	GTTTACCCCGTTCATTGTTGGTTCCTCAATGCTTATTAACAACTGATAGTTGTTGGCCT	420		
OY 1318	tcattatccttcgaagagtcataactcggagtttcgagtaattccttcctcagtgt	1377		
DB 421	CTTCCGCCAGCGCGGATGGGATATAGATGAGAGGAAATATGGGTGTTAATGCTTGGGTG	480		
OY 1378	gcaaatcaacccctttctccatctcgtcttgg	1411		
DB 481	GCAATCAAGGCCCACTTATCGACACCTGAGAGTGG	514		
RESULT 7				
AW726448	standard; RNA; EST; 679 BP.			
ID AW726448				
AC AW726448;				
XX AW726448.1				
SV				
XX 24-APR-2000 (Rel. 63, Created)				
XX 18-NOV-2000 (Rel. 65, Last updated, Version 2)				
DE GA_Ea0021l07 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum				
XX CDNA clone GA_Ea0021l07, mRNA sequence.				
XX				
XX EST.				

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XX Gossypium arboreum
OS Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Malvales; Malvaceae; Gossypium.
XX
XX [1]
XX 1-679
XX
XX Wang R.A., Frisch D., Yu Y., Main D., Rambo T., Simmons J., Henry D.,
XX Wood T.C., Leslie A., Wilkins T.A.;
XX "An integrated analysis of the genetics, development, and evolution of the
XX cotton fiber";
XX unpublished.
XX
XX
XX Contact: Ming RA
XX Clemson University Genomics Institute
XX
XX 100 Jordan Hall, Clemson, SC 29634, USA
XX
XX Tel: 864 656 7288
XX Fax: 864 656 4293
XX
XX Email: rwing@clemson.edu
XX
XX High quality sequence stop: 679.
XX
XX
XX Key Location/Qualifiers
XX
XX source 1..679
XX /db_xref="taxon:29729"
XX /db_xref="ESTLIB:2480"
XX /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
XX /organism="Gossypium arboreum"
XX /strain="AKA"
XX /cultivar="8400"
XX /clone="GA_Ea0021107"
XX /clone_id="Gossypium arboreum 7-10 dpa fiber library"
XX /tissue_type="Fibers isolated from bolls harvested 7-10
XX dpa"
XX /lab_host="E. coli"
XX
XX
XX Sequence 679 BP; 155 A; 124 C; 225 G; 175 T; 0 other:

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Query Match 6.1%; Score 106; DB 76; Length 679;
Best Local Similarity 50.4%; Pred. No. 1.4e-14;
Matches 259; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

Oy 898 tgaacacctagatcaactggttttctaccacccgctttaaagaacgcgaa 957
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9 TGAAGTACTAGCGGTGAACGCTGTTTCGAGCTTCATCCCTTGTTAGCTGCACGCGGTG 68

Oy 958 gttaaagatttttgcataaggttaagtcataagaccctaaattgttacaatcgcg 1017
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 GATCGAAAAGTTGTTCTCTATTAAAGCATGAACCAAGATTGTCACGGTTGTGA 128

Oy 1018 gaagaagaacaatacaatcctctctttttaaagaattcatcgagcggttgatga 1077
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 ACAAGAACCGATCAACAACGGTCTGTTTCTTAGACCGTTTACTGAAGCTCTCCATTA 188

Oy 1078 ttatacagctggttgcatactgaagtcatactgacacgggttagtcgagagaagat 1137
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 TTAATTCACCTTTTCAGCTGTTTGGAAGGTTTCGGGGTGGCCGACGAGTCAAGACT 248

Oy 1138 gacagtgaaacaagtgtgttgagagagagatgtgtatcgttcgatgagaaga 1197
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 GCGTATGTCCAGATTATCTTAGAGAAAGATTTGTAACTGTGCTTGTGAAGGAT 308

Oy 1198 taaagaagaagaacatacattagatcatcagggaaagttatgttgaagatgtg 1257
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 GGACCGAGTTGAGCGACACGAGCCGCTACATCAGTGGAGAACTCGATGGAACGCGCG 368

Oy 1258 attagtaatgttccttaagcccttgcataatcaacaagaactctctttagagat 1317
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 GTTAGCCCTGTCTATTTGGTTCGAATGCTTAAACAAGTACTAGTATGTTGGCCCT 428

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Oy 1318 tcattatcctctgaagagctatacactcgagtttcgatacttctcttagtg 1377
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 429 CTTCGCCACGCGCGATGTAGAGTGGAGACAAATATAGGTATTATGCTTTGGGTG 488

Oy 1378 gaaaatacaaccttttccatctgcttgg 1411
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 489 GCATPACAAGCCACTTATCGACACCTGAGGTTGG 522

RESULT 8
AM736058/c 534 bp mRNA EST 07-SEP-2000
LOCUS EST332044 KV3 Medicago truncatula cDNA clone PKV3-503, mRNA
DEFINITION
ACCESSION AM736058
VERSION AM736058.1 GI:7642902
KEYWORDS EST.
SOURCE Medicago truncatula
ORGANISM Medicago truncatula
barel medic.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.
1 (bases 1 to 534)
Vandenbosch, K., Hurt, J., Moore, J., Beremand, P., Peng, H., Ellis, L.,
Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and
Fraser, C.M.
ESTs from roots of Medicago truncatula after Rhizobium inoculation
Unpublished (1999)
Contact: Vandenbosch K
Department of Biology
Texas A&M University
College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
Email: kate@mail.bio.tamu.edu
Texas A&M EST name: T254173e
TIGR sequence name: MTEA86TK
More information is available at:
'http://chrysis.tamu.edu/medicago'
Seq primer: SKmod (CTA gaa cta gtc gat cc).

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FEATURES
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Location/Qualifiers
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="PKV3-503"
/clone_id="KV3"
/tissue_type="Seedling roots"
/dev_stage="3 days post-inoculation with Sinorhizobium
mellioli"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA
was directionally ligated into the Unizap XR vector from
stratagene and packaged using GigaPack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
BASE COUNT 142 a 133 c 86 g 173 t
ORIGIN

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Query Match 6.1%; Score 105.6; DB 120; Length 534;
Best Local Similarity 60.4%; Pred. No. 1.7e-14;
Matches 174; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Oy 977 aggttaagtcataagaccctaaattgttacaatcgaggaagaagcaatcatatc 1036
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Db 534 ATGTTAAGAGCCTTAATCAAACTTGTACAGTTGTGAACAAGCGTGAACAACAAC 475

Oy 1037 catcctctttttaaagaattcatcgagcggttgatattatcacagctgtgtgat 1096
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 474 ACTGCCCATTTCTTCNAAGATTTGTGAAGCTTACATTAAGTCTGCTGTTGAG 415

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BASE COUNT      134 a      97 c      118 g      120 t
ORIGIN
Query Match      5.9%; Score 102; DB 24; Length 469;
Best Local Similarity 57.5%; Pred. No. 1.2e-13;
Matches 183; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Oy 969 ttgtgcatagggttaagtcacatgaacccctaaattgttaccatcgcgagagaagaa 1028
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 77 TTTTGAGATTGCTGTAAGGTCACCTTTCTCCCAAGGTGACCAATGCGTGAGCAATCA 136

Oy 1029 atcataaccatccctcttttttaccagaatcatcagagcggttgattattatacagctg 1088
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 ACACAAACACAAACCCCTTCTTCAACAGGTTCAATGAAACCTTGATTAATCTTGCA 196

Oy 1089 tgttgattcactggaagctacatgcaccggtgagtcgagagagatgacagtgaac 1148
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 TCTTTGAGTCCATTGATGTCACCCCTCCCAAGACAGACAGAGAGATTAATGTGAGAC 256

Oy 1149 aagtggtttgggagagagattgtgatcgttgcgatggagagataaagaaag 1208
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 257 AACATTGCTGGCCAGGATATGTCATATCATCTTGTCGAAGCAAGAAAGCGTTG 316

Oy 1209 aaagacatgaaggttgatcatcgttgagagagattgttgagagttgattagtaag 1268
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 317 AGAGACATGAACTGTTCGCCGAAGTGGAAGTCAAGCTTAAGATGCGCGCTTCAGCAAT 376

Oy 1269 ttgctttaagccctttg 1286
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 377 GTCCCTTGAGTTCTTATG 394

RESULT 14
AM102078      495 bp      mRNA      EST      17-JUL-2000
LOCUS      s682903.y1 Gm-cl1009 glycine max cDNA clone GENOME SYSTEMS CLONE ID:
DEFINITION      Gm-cl1009-941 5' similar to TR:023566 023566 SCARECROW HOMOLOG. ;,
      mRNA sequence.
ACCESSION      AM102078
VERSION      AM102078.1 GI:6072691
KEYWORDS      soybean.
SOURCE      Glycine max
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
      Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE      1 (bases 1 to 495)
AUTHORS      Shoemaker,R., Kelm,P., Vodka,L., Erpelting,J., Coryell,V., Khanna
      ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C.,
      Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
      ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
      ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
      ,R., Waterston,R. and Wilson,R.
      Public Soybean EST Project
      Unpublished (1999)
TITLE      JOURNAL.
COMMENT      Contact: Shoemaker R/Public Soybean EST Project
      Public Soybean EST Project
      Washington University School of Medicine
      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
      Tel: 314 286 1800
      Fax: 314 286 1810
      Email: est@wustl.edu
      This clone is available through: Genome Systems, Inc. 4633 World
      Parkway Circle St. Louis, Missouri 63134 For further information
      call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
      427-3324 or contact: clones@genomesystems.com or
      info@genomesystems.com web site: www.genomesystems.com
      Insert Length: 708 Std Error: 0.00
      Seq primer: -40RP from Gldoo
      High quality sequence stop: 408.
      Location/Qualifiers

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/clone_1id="Gm-cl1009"
/lab_host="XLI0-Gold"
/note="Vector: pBluescript II XE; Site.1: EcoRI; Site.2:
XhoI; The mRNA was isolated from entire roots of
2-month-old 'Williams' plants that were greenhouse grown
in 5-gallon pots. To suppress nodulation, Black Gold
All-Purpose potting soil was supplemented with: 0.36g/L
available phosphoric acid (P205), 20mg/L urea N, 0.16g/L
S, 0.49mg/L B, 2.5mg/L Cu, 0.15g/L Fe, 13.53mg/L Mn,
0.26mg/L Mo, 14mg/L Zn, 20mg/L Ca, and the following
nutrients in a slow-release form (Osmocote): 0.165g/L
ammonia N, 0.185g/L nitrate N, 0.35g/L available
phosphoric acid, and 0.35g/L soluble potash. No nodules
were visible on the roots at harvest. Stragene's cDNA
Synthesis Kit (catalog #200401) was used to synthesize the
cDNA. First-strand synthesis was performed with 5-methyl
dCTP, hence the ligated cDNA is hemimethylated.
Stragene's first-strand synthesis primer was used
(AGAGAGAGAGAGAGAGAGACTGCTCGAG(T)-18). After
second-strand synthesis is, the cDNA ends were 'polished'
with clone Pfu DNA polymerase, ligated to EcoRI adapters,
and phosphorylated. The XhoI site within the first-strand
synthesis primer was restricted by digestion with XhoI;
all XhoI sites in the cDNA would be protected by their
hemimethylated status. The cDNA constructs were
size-fractionated with a 400bp cutoff, using a SizeSep 400
Spin column from Pharmacia. The column eluent was then
ligated into Stragene's pBluescript II XR predigested
vector (pBluescript II SK(+)) that had been digested with
EcoRI and XhoI, and phosphorylated. Both the white and
blue colonies appear to contain recombinant plasmids with
cDNA inserts. This library was constructed by Dr. Paul
Kelm and Dr. Virginia Coryell."

BASE COUNT      138 a      101 c      128 g      128 t
ORIGIN
Query Match      5.9%; Score 102; DB 11; Length 495;
Best Local Similarity 57.5%; Pred. No. 1.2e-13;
Matches 183; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

Oy 969 ttgtgcatagggttaagtcacatgaacccctaaattgttaccatcgcgagagaagaa 1028
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 101 TTTTGAGATTGCTGTAAGGTCACCTTTCTCCCAAGTGACCAATGCGTGAGAGCAATCA 160

Oy 1029 atcataaccatccctcttttttaccagaatcatcagagcggttgattattatacagctg 1088
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 161 ACACAAACACAAACCCCTTCTTCAACAGGTTCAATGAAACCTTGATTAATCTTGCA 220

Oy 1089 tgttgattcactggaagctacatgcaccggtgagtcgagagagatgacagtgaac 1148
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 221 TCTTTGAGTCCATTGATGTCACCCCTCCCAAGACAGACAGAGAGATTAATGTGAGAC 280

Oy 1149 aagtggtttgggagagagattgtgatcgttgcgatggagagataaagaaag 1208
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 281 AACATTGCTGGCCAGGATATGTCATATCATCTTGTCGAAGCAAGAAAGCGTTG 340

Oy 1209 aaagacatgaaggttgatcatcgttgagagagattgttgagagttgattagtaag 1268
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 341 AGAGACATGAACTGTTCGCCGAAGTGGAAGTCAAGCTTAAGATGCGCGCTTCAGCAAT 400

Oy 1269 ttgctttaagccctttg 1286
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 401 GTCCCTTGAGTTCTTATG 418

RESULT 15
AM119464      497 bp      mRNA      EST      17-JUL-2000
LOCUS      AM119464

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